

0590

07/31 OIPE
#2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/839,894

DATE: 08/07/2001

TIME: 11:40:45

Input Set : D:\seqlist.txt

Output Set: N:\CRF3\08072001\I839894.raw

4 <110> APPLICANT: Altboum, Zeev
5 Barry, Eileen M.
6 Levine, Myron M.
8 University of Maryland
10 <120> TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF THE
11 CSA OPERON
13 <130> FILE REFERENCE: UOFMD.006A
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/839,894 *OK*
C--> 15 <141> CURRENT FILING DATE: 2001-04-20
15 <150> PRIOR APPLICATION NUMBER: 60/198,626
16 <151> PRIOR FILING DATE: 2000-04-20
18 <160> NUMBER OF SEQ ID NOS: 40
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 717
24 <212> TYPE: DNA
25 <213> ORGANISM: E. coli
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)...(717) *✓*
31 <400> SEQUENCE: 1
32 atg cat aaa tta ttt tgt tta cta agt tta ctc ata act cca ttt gtt 48
33 Met His Lys Leu Phe Cys Leu Leu Ser Leu Leu Ile Thr Pro Phe Val
34 1 5 10 15
36 gca aat gca aac ttt atg ata tat cca ata tca aaa gat tta aag aat 96
37 Ala Asn Ala Asn Phe Met Ile Tyr Pro Ile Ser Lys Asp Leu Lys Asn
38 20 25 30
40 gga aat agc gag tta att cgt gtt tat tca aaa tca aaa gag ata caa 144
41 Gly Asn Ser Glu Leu Ile Arg Val Tyr Ser Lys Ser Lys Glu Ile Gln
42 35 40 45
44 tat ata aaa ata tat aca aaa aag att att aat ccc ggc aca act gaa 192
45 Tyr Ile Lys Ile Tyr Thr Lys Lys Ile Ile Asn Pro Gly Thr Thr Glu
46 50 55 60
48 gaa cat gaa gtt gat atg ccc aat tgg gat ggt ggg ttt gta gtt act 240
49 Glu His Glu Val Asp Met Pro Asn Trp Asp Gly Gly Phe Val Val Thr
50 65 70 75 80
52 cct caa aaa gtt att ctt cct gca gga ggg agt aaa tca ata cgt tta 288
53 Pro Gln Lys Val Ile Leu Pro Ala Gly Gly Ser Lys Ser Ile Arg Leu
54 85 90 95
56 act caa ttt aga ata cca aaa aaa gag gaa att tat aga gta tat ttt 336
57 Thr Gln Phe Arg Ile Pro Lys Lys Glu Glu Ile Tyr Arg Val Tyr Phe
58 100 105 110
60 gag gcg gta aaa cca gat agc aaa gaa aat gta att gat aat aaa aaa 384
61 Glu Ala Val Lys Pro Asp Ser Lys Glu Asn Val Ile Asp Asn Lys Lys
62 115 120 125
64 cta aca aca gag cta tct gtt aat ata att tat gcg gct cta atc aga 432
65 Leu Thr Thr Glu Leu Ser Val Asn Ile Ile Tyr Ala Ala Leu Ile Arg

ENTERED

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66      130      135      140
68 tct tta cca agt gaa caa aac ata tca cta aac att tct aga aat gca 480
69 Ser Leu Pro Ser Glu Gln Asn Ile Ser Leu Asn Ile Ser Arg Asn Ala
70 145      150      155      160
72 aga aaa aat ata att att tat aat aat ggg aat gtt aga gca ggt gtt 528
73 Arg Lys Asn Ile Ile Ile Tyr Asn Asn Gly Asn Val Arg Ala Gly Val
74      165      170      175
76 aaa gat att tat ttt tgt aag tca tct aat atc gat gat agc tgt gta 576
77 Lys Asp Ile Tyr Phe Cys Lys Ser Ser Asn Ile Asp Asp Ser Cys Val
78      180      185      190
80 aaa aaa acg cat aac aag aat ata tat cca gaa aag tca ttt gat acg 624
81 Lys Lys Thr His Asn Lys Asn Ile Tyr Pro Glu Lys Ser Phe Asp Thr
82      195      200      205
84 ctg gtt aat aac aat ttt tct tat gtt ttc att aaa tta aac cat gaa 672
85 Leu Val Asn Asn Asn Phe Ser Tyr Val Phe Ile Lys Leu Asn His Glu
86      210      215      220
88 gac ata gaa aaa gag caa gga cta ata caa tta aaa gtt cct tga 717
89 Asp Ile Glu Lys Glu Gln Gly Leu Ile Gln Leu Lys Val Pro *
90 225      230      235
94 <210> SEQ ID NO: 2
95 <211> LENGTH: 238
96 <212> TYPE: PRT
97 <213> ORGANISM: E. coli
99 <400> SEQUENCE: 2
100 Met His Lys Leu Phe Cys Leu Leu Ser Leu Leu Ile Thr Pro Phe Val
101 1      5      10      15
102 Ala Asn Ala Asn Phe Met Ile Tyr Pro Ile Ser Lys Asp Leu Lys Asn
103      20      25      30
104 Gly Asn Ser Glu Leu Ile Arg Val Tyr Ser Lys Ser Lys Glu Ile Gln
105      35      40      45
106 Tyr Ile Lys Ile Tyr Thr Lys Lys Ile Ile Asn Pro Gly Thr Thr Glu
107      50      55      60
108 Glu His Glu Val Asp Met Pro Asn Trp Asp Gly Gly Phe Val Val Thr
109 65      70      75      80
110 Pro Gln Lys Val Ile Leu Pro Ala Gly Gly Ser Lys Ser Ile Arg Leu
111      85      90      95
112 Thr Gln Phe Arg Ile Pro Lys Lys Glu Glu Ile Tyr Arg Val Tyr Phe
113      100      105      110
114 Glu Ala Val Lys Pro Asp Ser Lys Glu Asn Val Ile Asp Asn Lys Lys
115      115      120      125
116 Leu Thr Thr Glu Leu Ser Val Asn Ile Ile Tyr Ala Ala Leu Ile Arg
117      130      135      140
118 Ser Leu Pro Ser Glu Gln Asn Ile Ser Leu Asn Ile Ser Arg Asn Ala
119 145      150      155      160
120 Arg Lys Asn Ile Ile Ile Tyr Asn Asn Gly Asn Val Arg Ala Gly Val
121      165      170      175
122 Lys Asp Ile Tyr Phe Cys Lys Ser Ser Asn Ile Asp Asp Ser Cys Val
123      180      185      190
124 Lys Lys Thr His Asn Lys Asn Ile Tyr Pro Glu Lys Ser Phe Asp Thr

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125          195          200          205
126 Leu Val Asn Asn Asn Phe Ser Tyr Val Phe Ile Lys Leu Asn His Glu
127          210          215          220
128 Asp Ile Glu Lys Glu Gln Gly Leu Ile Gln Leu Lys Val Pro
129 225          230          235
132 <210> SEQ ID NO: 3
133 <211> LENGTH: 504
134 <212> TYPE: DNA
135 <213> ORGANISM: E. coli
137 <220> FEATURE:
138 <221> NAME/KEY: CDS
139 <222> LOCATION: (1)...(504) ✓
141 <400> SEQUENCE: 3
142 atg aaa tta aaa aaa act att ggt gca atg gca ctg acc aca atg ttt 48
143 Met Lys Leu Lys Lys Thr Ile Gly Ala Met Ala Leu Thr Thr Met Phe
144 1          5          10          15
146 gta gct atg agt gct tct gca gta gag aaa aat atc act gta aca gct 96
147 Val Ala Met Ser Ala Ser Ala Val Glu Lys Asn Ile Thr Val Thr Ala
148          20          25          30
150 agt gtt gat cct aca att gat att ttg caa gct gat ggt agt agt tta 144
151 Ser Val Asp Pro Thr Ile Asp Ile Leu Gln Ala Asp Gly Ser Ser Leu
152          35          40          45
154 cct act gct gta gaa tta acc tat tca cct gcg gca agt cgt ttt gaa 192
155 Pro Thr Ala Val Glu Leu Thr Tyr Ser Pro Ala Ala Ser Arg Phe Glu
156          50          55          60
158 aat tat aaa atc gca act aaa gtt cat aca aat gtt ata aat aaa aat 240
159 Asn Tyr Lys Ile Ala Thr Lys Val His Thr Asn Val Ile Asn Lys Asn
160 65          70          75          80
162 gta cta gtt aag ctt gta aat gat cca aaa ctt aca aat gtt ttg gat 288
163 Val Leu Val Lys Leu Val Asn Asp Pro Lys Leu Thr Asn Val Leu Asp
164          85          90          95
166 tct aca aaa caa ctc ccc att act gta tca tat gga gga aag act cta 336
167 Ser Thr Lys Gln Leu Pro Ile Thr Val Ser Tyr Gly Gly Lys Thr Leu
168          100          105          110
170 tca acc gca gat gtg act ttt gaa cct gca gaa tta aat ttt gga acg 384
171 Ser Thr Ala Asp Val Thr Phe Glu Pro Ala Glu Leu Asn Phe Gly Thr
172          115          120          125
174 tca ggt gta act ggt gta tct tct tcc caa gat tta gtg att ggt gcg 432
175 Ser Gly Val Thr Gly Val Ser Ser Ser Gln Asp Leu Val Ile Gly Ala
176          130          135          140
178 act aca gca caa gca cca acg gcg gga aat tat agt ggg gtc gtt tct 480
179 Thr Thr Ala Gln Ala Pro Thr Ala Gly Asn Tyr Ser Gly Val Val Ser
180 145          150          155          160
182 atc tta atg acc tta gca tca taa 504
183 Ile Leu Met Thr Leu Ala Ser *
184          165
187 <210> SEQ ID NO: 4
188 <211> LENGTH: 167
189 <212> TYPE: PRT

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190 <213> ORGANISM: E. coli
192 <400> SEQUENCE: 4
193 Met Lys Leu Lys Lys Thr Ile Gly Ala Met Ala Leu Thr Thr Met Phe
194 1 5 10 15
195 Val Ala Met Ser Ala Ser Ala Val Glu Lys Asn Ile Thr Val Thr Ala
196 20 25 30
197 Ser Val Asp Pro Thr Ile Asp Ile Leu Gln Ala Asp Gly Ser Ser Leu
198 35 40 45
199 Pro Thr Ala Val Glu Leu Thr Tyr Ser Pro Ala Ala Ser Arg Phe Glu
200 50 55 60
201 Asn Tyr Lys Ile Ala Thr Lys Val His Thr Asn Val Ile Asn Lys Asn
202 65 70 75 80
203 Val Leu Val Lys Leu Val Asn Asp Pro Lys Leu Thr Asn Val Leu Asp
204 85 90 95
205 Ser Thr Lys Gln Leu Pro Ile Thr Val Ser Tyr Gly Gly Lys Thr Leu
206 100 105 110
207 Ser Thr Ala Asp Val Thr Phe Glu Pro Ala Glu Leu Asn Phe Gly Thr
208 115 120 125
209 Ser Gly Val Thr Gly Val Ser Ser Ser Gln Asp Leu Val Ile Gly Ala
210 130 135 140
211 Thr Thr Ala Gln Ala Pro Thr Ala Gly Asn Tyr Ser Gly Val Val Ser
212 145 150 155 160
213 Ile Leu Met Thr Leu Ala Ser
214 165
217 <210> SEQ ID NO: 5
218 <211> LENGTH: 2604
219 <212> TYPE: DNA
220 <213> ORGANISM: E. coli
222 <220> FEATURE:
223 <221> NAME/KEY: CDS
224 <222> LOCATION: (1)...(2604)
226 <400> SEQUENCE: 5
227 atg aca aaa aaa aat aca tta tat ata acg atc atc gca atg cta act 48
228 Met Thr Lys Lys Asn Thr Leu Tyr Ile Thr Ile Ile Ala Met Leu Thr
229 1 5 10 15
231 cca tat tca gtt ttt tcc gga gat ata ccc aac tct ttc cgt gat tta 96
232 Pro Tyr Ser Val Phe Ser Gly Asp Ile Pro Asn Ser Phe Arg Asp Leu
233 20 25 30
235 tgg gga gaa caa gat gaa ttt tat gaa gta aaa cta tat gga caa act 144
236 Trp Gly Glu Gln Asp Glu Phe Tyr Glu Val Lys Leu Tyr Gly Gln Thr
237 35 40 45
239 cta gga ata cat cga att aaa aca acc cca aca cat att aag ttt tat 192
240 Leu Gly Ile His Arg Ile Lys Thr Thr Pro Thr His Ile Lys Phe Tyr
241 50 55 60
243 tca ccc gaa agc att tta gat aaa ata aat gta aaa gaa aag gaa 240
244 Ser Pro Glu Ser Ile Leu Asp Lys Ile Asn Val Lys Lys Glu Lys Glu
245 65 70 75 80
247 aag aaa ttg agt gtt ttg ttc act aat tct ttt tca aga aat ggc aat 288
248 Lys Lys Leu Ser Val Leu Phe Thr Asn Ser Phe Ser Arg Asn Gly Asn

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249		85		90		95		
251	atg agt tgt	cag ggg aat gct act	ata cag tat aac tgc aat tac att	336				
252	Met Ser Cys	Gln Gly Asn Ala Thr	Ile Gln Tyr Asn Cys Asn Tyr Ile					
253		100	105	110				
255	aaa aca aaa	tca gta gat gtc atc gtt gat gat gtt gat aat gtt gtt	384					
256	Lys Thr Lys	Ser Val Asp Val	Ile Val Asp Asp Val Asp Asn Val Val					
257		115	120	125				
259	aac ctt ttt	ata ggt aat gaa ttt ctg gat tct gaa gca cac aat gat	432					
260	Asn Leu Phe	Ile Gly Asn Glu Phe Leu Asp Ser	Glu Ala His Asn Asp					
261		130	135	140				
263	gaa tat cat	caa tta tca cga aat gta aaa aaa gct ttt ata caa agc	480					
264	Glu Tyr His	Gln Leu Ser Arg Asn Val Lys Lys Ala Phe Ile Gln Ser						
265	145	150	155	160				
267	cag aca att	aat gtc tca gat tct ggg aag tat aaa agt ttg tct gtt	528					
268	Gln Thr Ile	Asn Val Ser Asp Ser Gly Lys Tyr Lys Ser Leu Ser Val						
269		165	170	175				
271	tca ggg aat	agc gcg ctg ggt att aca gat aca agt tat gct gtc tta	576					
272	Ser Gly Asn	Ser Ala Leu Gly Ile Thr Asp Thr Ser Tyr Ala Val Leu						
273		180	185	190				
275	aat tgg tgg	atg aat tac aat aaa ttt aat ggt tac agc aac aac gaa	624					
276	Asn Trp Trp	Met Asn Tyr Asn Lys Phe Asn Gly Tyr Ser Asn Asn Glu						
277		195	200	205				
279	aga aca atc	aat agt ttg tac ttt aga cat gat tta gat aag aga tat	672					
280	Arg Thr Ile	Asn Ser Leu Tyr Phe Arg His Asp Leu Asp Lys Arg Tyr						
281		210	215	220				
283	tat tat caa	ttt gga cga atg gat cgt aca gat ttg tca caa agt att	720					
284	Tyr Tyr Gln	Phe Gly Arg Met Asp Arg Thr Asp Leu Ser Gln Ser Ile						
285	225	230	235	240				
287	agc ggg aac	ttt aat ttt aac tta ctt cct tta ccc gat att gat ggt	768					
288	Ser Gly Asn	Phe Asn Phe Asn Leu Leu Pro Leu Pro Asp Ile Asp Gly						
289		245	250	255				
291	ata agg aca	gga acc aca caa tct tat atc aaa aat aca gat aag ttt	816					
292	Ile Arg Thr	Gly Thr Thr Gln Ser Tyr Ile Lys Asn Thr Asp Lys Phe						
293		260	265	270				
295	atc gca tcc	cct gta act gtt atg tta act aat ttt tcc aga gtg gaa	864					
296	Ile Ala Ser	Pro Val Thr Val Met Leu Thr Asn Phe Ser Arg Val Glu						
297		275	280	285				
299	gct ttt cgc	aat aat caa tta ttg ggc gta tgg tat tta gat tct gga	912					
300	Ala Phe Arg	Asn Asn Gln Leu Leu Gly Val Trp Tyr Leu Asp Ser Gly						
301		290	295	300				
303	gta aat gaa	tta gat aca gct cgt tta cct tat ggt agt tac gat ctt	960					
304	Val Asn Glu	Leu Asp Thr Ala Arg Leu Pro Tyr Gly Ser Tyr Asp Leu						
305	305	310	315	320				
307	aaa tta aaa	att ttt gaa aat act cag tta gtt cgt gaa gaa ata att	1008					
308	Lys Leu Lys	Ile Phe Glu Asn Thr Gln Leu Val Arg Glu Glu Ile Ile						
309		325	330	335				
311	cct ttt aat	aaa ggg aga agt tct att ggt gat atg caa tgg gac gtt	1056					
312	Pro Phe Asn	Lys Gly Arg Ser Ser Ile Gly Asp Met Gln Trp Asp Val						
313		340	345	350				

VERIFICATION SUMMARY

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Output Set: N:\CRF3\08072001\I839894.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:990 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 27, CDS LOCATION:283..999
L:1054 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 27, CDS
LOCATION:1028..1531
L:1098 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 27, CDS
LOCATION:1589..4192
L:1418 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 27, CDS
LOCATION:5790..6119